## SEQUENCE LISTING

```
<110> FUKUCHI, Naoyuki
     FUTAKI, Fumie
     KITO, Morikazu
     SATO, Seiichi
     KAJIURA, Takayuki
     ONO, Yukitsugu
     TANAKA,, Akiko
     SHINOZAKI, Junko
<120> Substance with Antithrombic Activity and Method for Detecting
Glycocalicin
<130> 198804US0PCT
<140> US 09/673,245
<141> 2000-10-23
<150> PCT/JP99/00089
<151> 1998-01-13
<150> JP 10-113962
<151> 1998-04-23
<160> 14
<170> PatentIn version 3.1
<210> 1
<211> 29
<212> DNA
<213> ARTIFICIAL SEQUENCE
<220>
<223> SYNTHETIC DNA
<400> 1
atatctagat gtgcccaggg attgtggtt
                                                                      29
<210>
      2
<211>
      36
<212> DNA
<213> ARTIFICIAL SEQUENCE
<220>
<223>
      SYNTHETIC DNA
                                                                      36
ataaagcttc tcgagtcatt taccaggaga gtggga
      3
<210>
<211>
      36
<212>
      DNA
```

<213> ARTIFICIAL SEQUENCE

<220> <223>		NTHE:	ric 1	DNA												
<400> ataaa	3 igctt	c to	gagt	catt	tac	cagg	aga	gtgg	gga					•	-	36
<210 × <211 × <212 × <213 ×	> 68 > DN		scul	.us												
<220: <221: <222: <223	> CI > (:	os 1)(	(684)	1												
<400 gtg Val 1		agg g Arg i	Asp (	tgt ( Cys (	ggt ( Gly (	tgt Cys	aag Lys	cct Pro	tgc Cys 10	ata Ile	tgt Cys	aca Thr	gtc Val	cca Pro 15	gaa Glu	48
gta Val	tca Ser	tct ( Ser	gtc Val 20	ttc Phe	atc Ile	ttc Phe	ccc Pro	cca Pro 25	aag Lys	ccc Pro	aag Lys	gat Asp	gtg Val 30	ctc Leu	acc Thr	96
att Ile	act Thr	ctg Leu 35	act Thr	cct Pro	aag Lys	gtc Val	acg Thr 40	tgt Cys	gtt Val	gtg Val	gta Val	gac Asp 45	atc Ile	agc Ser	aag Lys	144
gat Asp	gat Asp 50	ccc Pro	gag Glu	gtc Val	cag Gln	ttc Phe 55	agc Ser	tgg Trp	ttt Phe	gta Val	gat Asp 60	gat Asp	gtg Val	gag Glu	gtg Val	192
cac His 65	aca Thr	gct Ala	cag Gln	acg Thr	caa Gln 70	ccc Pro	cgg Arg	gag Glu	gag Glu	cag Gln 75	ttc Phe	aac Asn	agc Ser	act Thr	ttc Phe 80	240
cgc Arg	tca Ser	gtc Val	agt Ser	Glu	ctt Leu	Pro	ше	atg Met	cac His 90	cag Gln	gac Asp	tgg Trp	ctc Leu	aat Asn 95	ggc Gly	288
aag Lys	gag Glu	ttc Phe	aaa Lys 100	tgc Cys	agg Arg	gta Val	aac Asn	agt Ser 105	ATa	gct Ala	ttc Phe	cct Pro	gcc Ala 110		atc Ile	336
gag Glu	aaa Lys	acc Thr	Ile	tcc Ser	aaa Lys	acc	aaa Lys 120	; GIZ	aga Arc	ccg Pro	aag Lys	gct Ala 125	110	cag Gln	gtg Val	384
tac Tyr	aco Thr	: Ile	cca Pro	cct Pro	ccc Pro	aag Lys 135	s GIL	g cag ı Glı	g atg n Met	g gcc	aag Lys 140	, Aor	aaa Lys	gtc Val	agt Ser	432
cto	g aco	tgc	ato	g ata	a aca	a ga	e tto	c tto	c cct	gaa	a gad	att	act	gto	g gag	486

145	Met Ile	Thr Asp 150	Phe Phe	Pro Glu 155	Asp Ile	Thr	Val	Glu 160	
tgg cag tgg Trp Gln Trp									528
atc atg gac Ile Met Asp									576
cag aag agc Gln Lys Ser 195					_	Ser			624
cat gag ggc His Glu Gly 210									672
cct ggt aaa Pro Gly Lys 225	tga						÷.		684
<210> 5 <211> 227 <212> PRT <213> Mus n	nusculus								
<400> 5									
<pre>&lt;400&gt; 5  Val Pro Arg 1</pre>	Asp Cys 5	Gly Cys	Lys Pro	Cys Ile	Cys Thr	Val	Pro 15	Glu	
Val Pro Arg	5			10			15		
Val Pro Arg 1	Val Phe	Ile Phe	Pro Pro 25	10 Lys Pro	Lys Asp	Val 30	15 Leu	Thr	
Val Pro Arg  1  Val Ser Ser  Ile Thr Leu	Val Phe 20	Ile Phe	Pro Pro 25 Thr Cys 40	Lys Pro	Lys Asp Val Asp 45	Val 30	15 Leu Ser	Thr	
Val Pro Arg  Val Ser Ser  Ile Thr Leu 35  Asp Asp Pro	Val Phe 20 Thr Pro	Ile Phe Lys Val Gln Phe 55	Pro Pro 25 Thr Cys 40 Ser Trp	Lys Pro Val Val Phe Val	Lys Asp Val Asp 45 Asp Asp	Val 30 Ile Val	Leu Ser	Thr Lys Val	
Val Pro Arg 1  Val Ser Ser  Ile Thr Leu 35  Asp Asp Pro 50  His Thr Ala	Val Phe 20 Thr Pro Glu Val Gln Thr	Ile Phe Lys Val Gln Phe 55 Gln Pro 70	Pro Pro 25 Thr Cys 40 Ser Trp	Lys Pro Val Val Phe Val Glu Gln 75	Val Asp 45 Asp Asp 60	Val 30 Ile Val	Leu Ser Glu	Thr Lys Val Phe	

Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val

Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser 130 135 140

Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu 145 150 155 160

Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro 165 170 175

Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val 180 185 190

Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu 195 200 205

His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser 210 215 220

Pro Gly Lys 225

<210> 6

<211> 1689

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> SYNTHETIC DNA

<220>

<221> CDS

<222> (1)..(1686)

<223>

<220>

<221> sig\_peptide

<222> (1)..(48)

<223>

<220>

<221> mat\_peptide

<222> (49)..()

<400	)> (	5															
atg	cct	ctc												cac His			48
														gtg Val 15			96
														aaa Lys	gac Asp		144
						-				_				tcc Ser	_		192
														gat Asp			240
														ctg Leu			288
														cta Leu 95		•	336
														cgg Arg			384
														caa Gln			432
														ctc Leu			480
														aac Asn			528
act Thr	gag Glu	ctc Leu	ccc Pro	gct Ala 165	Gly 999	ctc Leu	ctg Leu	aat Asn	999 Gly 170	ctg Leu	gag Glu	aat Asn	ctc Leu	gac Asp 175	acc Thr		576
ctt Leu	ctc Leu	ctc Leu	caa Gln 180	gag Glu	aac Asn	tcg Ser	ctg Leu	tat Tyr 185	aca Thr	ata Ile	cca Pro	aag Lys	ggc Gly 190	ttt Phe	ttt Phe		624
999	tcc	cac	ctc	ctg	cct	ttt	ġct	ttt	ctc	cac	999	aac	ccc	tgg	tta		672

Gly S		His 195	Leu	Leu	Pro	Phe	Ala 200	Phe	Leu	His	Gl	y P	Asn 205	Pro	Trp	Ŀ	eu				
tgc a	aac Asn 210	tgt Cys	gag Glu	atc Ile	ctc Leu	tat Tyr 215	ttt Phe	cgt Arg	cgc Arg	tgg Trp	ct Le 22	-u \	ag Gln	gac Asp	aat Asn	g A	ct la	720			
gaa a Glu a 225	aat Asn	gtc Val	tac Tyr	gta Val	tgg Trp 230	aag Lys	caa Gln	ggt Gly	gtg Val	gac Asp 235		tc a	aag Lys	gcc Ala	at <u>c</u> Met	g a : T 2	cc hr 40	.768	3		
tct Ser	aac Asn	gtg Val	gcc Ala	agt Ser 245	gtg Val	cag Gln	tgt Cys	gac Asp	aat Asn 250	tca Ser	ga A	ac sp	aag Lys	ttt Phe	Pro 25!		tc al	816	5		
tac Tyr	aaa Lys	tac Tyr	cca Pro 260	Gly	aag Lys	G1y 999	tgc Cys	ccc Pro 265	1111	ctt Lei	g i G	gt ly	gat Asp	gaa Glu 270		t s	ac Asp	864	4		
aca Thr	gac Asp	cta Leu 275	Tyr	gat Asp	tac Tyr	tac Tyr	cca Pro	GIU	gag Glu	gao Asj	c a p T	ct hr	gag Glu 285	ggc	ga As	t a p 1	aag Lys	91	2		
gtg Val	cgt Arg 290	Ala	aca Thr	agg Arg	g act g Thr	gtg Val	. vai	aag Lys	tto Phe	e cc	0 1	acc Thr 300	aaa Lys	gcc	c ca a Hi	t i	aca Thr	96	0.		
acc Thr 305	ccc	tgg Trp	g ggt	cta / Let	a tto 1 Phe 310	e Tyi	tca Sei	tgg	g tco o Se:	ac r Th 31		gct Ala	tct Ser	cta Le	aga As	sp	gtg Val 320	100	8		
ccc Pro	agg Arg	gat Asp	tg Cy	t gg s Gl; 32	t tg y Cy 5	t aag s Ly:	g cc	t tgo	c atos Il	c cy	jt a 's '	aca Thr	gto Val	Pr	a ga o G: 3:	aa lu 35	gta Val	105	56		-
tca Ser	tct Sei	gto Vai	c tt l Ph 34	e Il	c tt e Ph	c cc e Pr	c cc o Pr	a aa o Ly 34	S PI	c aa	ag (	gat Asp	gto Val	ct Le 35	-	cc hr	att Ile	110	04		•
act Thr	cto	g ac u Th 35	r Pr	t aa o Ly	g gt s Va	c ac	g tg r Cy 36	s va	t gt .1 Va	g gt 1 Va	al	gac Asp	ato 110 36		c a r L	ag ys	gat Asp	11	52		
gat As <u>r</u>	cc Pr 37	o Gl	g gt u Va	c ca ll Gl	ıg tt .n Ph	c ag ne Se 37	er Tr	g tt p Ph	t gt ne Va	a ga	at sp	gat Asp 380	, ,,	g ga 1 Gl	ıg g .u V	tg al	cac His	12	00		
aca Th: 38	r Al	t ca a Gl	ıg ad .n Tl	eg ca ir Gi	ln Pi	cc co ro Ai	gg ga cg Gi	ag ga lu Gl	ag ca Lu Gi	L11 T	tc he 95	aac Ası	c ag n Se	c ac	et t	tc	cgc Arg 400	12	:48		
tc. Se	a gt r Va	c ag	gt ga er G	lu L	tt co eu P: 05	cc at	tc at le Mo	tg ca et H:	IS G	ag g ln A	ac sp	tg:	g ct p Le	c a	-	ggc 3ly 115	aag Lys	12	296	-	
ga Gl	g tt u Pì	c aa ne Ly	aa t ys C	gc a ys A	gg g rg V	ta a al A	ac a sn S	gt g er A	ca g la A	ct t la F	tc	cc Pr	t go o Al	ec c la P	cc a	atc Ile	gag Glu	13	344		
						•				6											

aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr 435 440 445	1392
acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu 450 455 460	1440
acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp 465 470 480	1488
cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile 485 490 495	1536
atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln 500 505 510	1584
aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His 515 520 525	1632
gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro 530 535 540	1680
ggt aaa tga Gly Lys 545	1689
<210> 7 <211> 562 <212> PRT <213> ARTIFICIAL SEQUENCE	
<220> <223> SYNTHETIC DNA	
<400> 7	
Met Pro Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro -15 -10 -5 -1	
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn 1 5 10 15	
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	

- Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu 35 40 45
- Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg 50 55
- Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly 65 70 75 80
- Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly 85 90 95
- Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu 100 105 110
- Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu 115 120 125
- Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu 130 135 140
- Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu 145 150 155 160
- Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr 165
- Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe 180 185 190
- Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu 195 200 205
- Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala 210 215 220
- Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr 225 230 235 240
- Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val 245 250 250
- Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp

260 265 270

Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys 275 280 285

Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr 290 295 300

Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val 305 310 315 320

Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
325 330 335

Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile 340 345 350

Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp 355 360 365

Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His 370 375 380

Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg 385 390 395 400

Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys 405 410 415

Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu 420 425 430

Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr 435 440 445

Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu 450 455 460

Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp 465 470 475 480

Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile 485 490 495

```
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
                       535
Gly Lys
545
<210> 8
<211> 30
<212> DNA
<213> ARTIFICIAL SEQUENCE
<220>
<223> SYNTHETIC DNA
<400> 8
agctaggatc cgagcccaga gggcccacaa
                                                                     30
<210> 9
<211> 45
<212> DNA
<213> ARTIFICIAL SEQUENCE
<220>
<223> SYNTHETIC DNA
<400> 9
cccaagette tegagacata cettteattt acceggagte eggga
                                                                     45
<210> 10
<211> 729
<212> DNA
<213> ARTIFICIAL SEQUENCE
<220>
<223> SNTHETIC DNA
<220>
<221> CDS
<222> (7)..(708)
<223>
```

Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln

<400> 10

ggatcc gag ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys 1 5 10	48
tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro 15 20 25 30	96
cca aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr 35 40 45	144
tgt gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser 50 55 60	192
tgg ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His 65 70 75	240
aga gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile 80 85 90	288
cag cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn 95 100 105 110	336
aac aaa gac ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys 115 120 125	384
ggg tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu 130 135 140	432
gag atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe 145 150 155	480
atg cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu 160 165 170	528
cta aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr 175 180 185 190	576
ttc atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg . 195 200 205	624
aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His 210 215 220	672
acg act aag agc ttc tcc cgg act ccg ggt aaa tga aaggtatgtc	718

Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys 225 230

tcgagaagct t 729

<210> 11

<211> 233

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> SNTHETIC DNA

<400> 11

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro 1 5 10 15

Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys 20 25 30

Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val
35 40 45

Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe 50 55 60

Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu 65 70 75 80

Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His 85 90 95

Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys 100 105 110

Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser 115 120 125

Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Met 130 135 140

Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro 145 150 155 160

Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn

175 170 165

Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met 185 180 Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser 195 200 Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr 220 215 210 Lys Ser Phe Ser Arg Thr Pro Gly Lys 230 225 <210> 12 <211> 30 <212> DNA <213> ARTIFICIAL SEQUENCE <220> <223> SYNTHETIC DNA <400> 12 30 agctatctag acgagcccag agggcccaca <210> 13 1707 <211> <212> DNA <213> ARTIFICIAL SEQUENCE <220> <223> SYNTHETIC DNA <220>

<221> CDS

<222> (1)..(1704)

<223>

<220>

<221> sig\_peptide

<222> (1)..(48)

<223>

<220>

<221> mat\_peptide

<222> (49)..()

<223>

cct			ttg Leu						48
			gtc Val						96
			ctg Leu						144
			ctg Leu						192
			tac Tyr						240
			ctc Leu 70						288
			cac His						336
			ctc Leu						384
			ggt Gly						432
	_		aat Asn	 _					480
			ctg Leu 150						528
			Gly aaa						576
			aac Asn						624
		_	cct Pro	_					672

tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala 210 215	720
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr 225 235 240	768
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val 245	816
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp 260 265 270	864
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys 275 280 285	912
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	960
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gag Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu 315 320	1008
ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala 325 330 335	1056
cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc Pro Asn Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile 340 345	1104
aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val 355 360 365	1152
gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val 370 375 380	1200
aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp 385 390 395 400	1248
tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln 405 410 415	1296
gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp 420 425 430	1344
ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta	1392

Leu Pro Ala Pro Ile Glu 435	Arg Thr Ile Ser I 440	Lys Pro Lys Gly Ser 445	Val
aga gct cca cag gta tat Arg Ala Pro Gln Val Tyr 450			
aag aaa cag gtc act ctg Lys Lys Gln Val Thr Leu 465 470	Thr Cys Met Val 7		
gac att tac gtg gag tgg Asp Ile Tyr Val Glu Trp 485			
aag aac act gaa cca gto Lys Asn Thr Glu Pro Val 500			
agc aag ctg aga gtg gaa Ser Lys Leu Arg Val Glu 515			
tcc tgt tca gtg gtc cac Ser Cys Ser Val Val His 530			
agc ttc tcc cgg act ccg Ser Phe Ser Arg Thr Pro 545 550			1707
<210> 14 <211> 568 <212> PRT <213> ARTIFICIAL SEQUE	NCE		
<220> <223> SYNTHETIC DNA			
<400> 14		· .	
Met Pro Leu Leu Leu -15	Leu Leu Leu Leu I -10	Pro Ser Pro Leu His	Pro -1
His Pro Ile Cys Glu Val	Ser Lys Val Ala S	Ser His Leu Glu Val 15	Asn
Cys Asp Lys Arg Asn Leu 20	Thr Ala Leu Pro I 25	Pro Asp Leu Pro Lys 30	Asp
Thr Thr Ile Leu His Leu 35	Ser Glu Asn Leu I	Leu Tyr Thr Phe Ser 45	Leu

- Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg 50 55 60
- Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
  65 70 75 80
- Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Gly 85 90 95
- Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu 100 105 110
- Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu 115 120 125
- Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu 130 135 140
- Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu 145 150 155 160
- Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr 165 170 175
- Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe 180 185 190
- Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu 195 200 205
- Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala 210 215 220
- Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr 225 230 235 240
- Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val 245 250 255
- Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp 260 265

- Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys 275 280 285
- Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr 290 295 300
- Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu 305 310 315
- Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala 325 330 335
- Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile 340 345 350
- Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val 355 360
- Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val 370 380
- Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp 385 390 395
- Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln 405 410 415
- Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp 420 425 430
- Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val
- Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr 450 455 460
- Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu 465 470 475 480
- Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr 485 490 495
- Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr

500 505 510

Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr 515 520 525

Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys 530 535 540

Ser Phe Ser Arg Thr Pro Gly Lys 545 550